

COPY

SEQUENCE LISTING

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Kavanaugh, W. Michael

<120> HUMAN FGF-21 GENE AND GENE EXPRESSION
PRODUCTS

<130> PP-16758.001/201130.408

<140> 09/715,805
<141> 2000-11-16

<160> 17

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<211> 659
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (14)...(646)

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 Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly
 1 5 10

ctg tgg gtc cga ctg ctg gct gtc ttc ctg ctg ggg gtc tac caa 97
Leu Trp Val Arg Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln
 15 20 25

gca tac ccc atc cct gac tcc agc ccc ctc ctc cag ttt ggg ggt caa 145
Ala Tyr Pro Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln
 30 35 40

gtc cgg cag agg tac ctc tac aca gat gac gac caa gac act gaa gcc 193
Val Arg Gln Arg Tyr Leu Tyr Asp Asp Asp Gln Asp Thr Glu Ala
 45 50 60

cac ctg gag atc agg gag gat gga aca gtg gta ggc gca gca cac cgc 241
His Leu Glu Ile Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg
 65 70 75

agt cca gaa agt ctc ctg gag ctc aaa gcc ttg aag cca ggg gtc att 289
Ser Pro Glu Ser Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile
 80 85 90

caa atc ctg ggt gtc aaa gcc tct agg ttt ctt tgc caa cag cca gat 337
Gln Ile Leu Gly Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp

95	100	105	
gga gct ctc tat gga tcg cct cac ttt gat cct gag gcc tgc agc ttc Gly Ala Leu Tyr Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe 110 115 120			
aga gaa ctg ctg ctg gag gac ggt tac aat gtg tac cag tct gaa gcc Arg Glu Leu Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala 125 130 135 140			
cat ggc ctg ccc ctg cgt ctg cct cag aag gac tcc cca aac cag gat His Gly Leu Pro Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp 145 150 155			
gca aca tcc tgg gga cct gtg cgc ttc ctg ccc atg cca ggc ctg ctc Ala Thr Ser Trp Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu 160 165 170			
cac gag ccc caa gac caa gca gga ttc ctg ccc cca gag ccc cca gat His Glu Pro Gln Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp 175 180 185			
gtg ggc tcc tct gac ccc ctg agc atg gta gag cct tta cag ggc cga Val Gly Ser Ser Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg 190 195 200			
agc ccc agc tat gcg tcc tga ctcttcctga atc Ser Pro Ser Tyr Ala Ser * 205 210			
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<400> 2 Met Glu Trp Met Arg Ser Arg Val Gly Thr Leu Gly Leu Trp Val Arg 1 5 10 15 Leu Leu Leu Ala Val Phe Leu Leu Gly Val Tyr Gln Ala Tyr Pro Ile 20 25 30			
Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg 35 40 45			
Tyr Leu Tyr Thr Asp Asp Gln Asp Thr Glu Ala His Leu Glu Ile 50 55 60			
Arg Glu Asp Gly Thr Val Val Gly Ala Ala His Arg Ser Pro Glu Ser 65 70 75 80			
Leu Leu Glu Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly 85 90 95			
Val Lys Ala Ser Arg Phe Leu Cys Gln Gln Pro Asp Gly Ala Leu Tyr 100 105 110			
Gly Ser Pro His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu 115 120 125			
Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro			

130	135	140
Leu Arg Leu Pro Gln Lys Asp Ser Pro Asn Gln Asp Ala Thr Ser Trp		
145	150	155
Gly Pro Val Arg Phe Leu Pro Met Pro Gly Leu Leu His Glu Pro Gln		160
165	170	175
Asp Gln Ala Gly Phe Leu Pro Pro Glu Pro Pro Asp Val Gly Ser Ser		
180	185	190
Asp Pro Leu Ser Met Val Glu Pro Leu Gln Gly Arg Ser Pro Ser Tyr		
195	200	205
Ala Ser		
210		

<210> 3
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (9)...(638)

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gtt tct gtg ctg gct ggt ctt ctg ctg gga gcc tgc cag gca cac ccc	98		
Val Ser Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro			
15	20	25	30

atc cct gac tcc agt cct ctc ctg caa ttc ggg ggc caa gtc cgg cag	146	
Ile Pro Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln		
35	40	45

cgg tac ctc tac aca gat gat gcc cag aca gaa gcc cac ctg gag	194	
Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu		
50	55	60

atc agg gag gat ggg acg gtg ggg ggc gct gct gac cag agc ccc gaa	242	
Ile Arg Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu		
65	70	75

agt ctc ctg cag ctg aaa gcc ttg aag ccg gga gtt att caa atc ttg	290	
Ser Leu Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu		
80	85	90

gga gtc aag aca tcc agg ttc ctg tgc cag cgg cca gat ggg gcc ctg	338		
Gly Val Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu			
95	100	105	110

tat gga tcg ctc cac ttt gac cct gag gcc tgc agc ttc cgg gag ctg	386	
Tyr Gly Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu		
115	120	125

ctt ctt gag gac gga tac aat gtt tac cag tcc gaa gcc cac ggc ctc		434	
Leu Leu Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu			
130	135	140	
ccg ctg cac ctg cca ggg aac aag tcc cca cac cgg gac cct gca ccc		482	
Pro Leu His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro			
145	150	155	
cga gga cca gct cgc ttc ctg cca cta cca ggc ctg ccc ccc gca ctc		530	
Arg Gly Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu			
160	165	170	
ccg gag cca ccc gga atc ctg gcc ccc cag ccc ccc gat gtg ggc tcc		578	
Pro Glu Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser			
175	180	185	190
tcg gac cct ctg agc atg gtg gga cct tcc cag ggc cga agc ccc agc		626	
Ser Asp Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser			
195	200	205	
tac gct tcc tga agcca		643	
Tyr Ala Ser *			

<210> 4
<211> 209
<212> PRT
<213> Homo sapiens

<400> 4			
Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser			
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Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro			
20	25	30	
Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr			
35	40	45	
Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His Leu Glu Ile Arg			
50	55	60	
Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu			
65	70	75	80
Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val			
85	90	95	
Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly			
100	105	110	
Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu			
115	120	125	
Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu			
130	135	140	
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly			
145	150	155	160
Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Leu Pro Glu			
165	170	175	

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
180 185 190
Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
195 200 205
Ser

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 5
agccattgtt ggactcgac

20

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 6
tggcttcagg aagcgttagct

20

<210> 7
<211> 16
<212> PRT
<213> Homo sapiens

<400> 7
Arg Gln Arg Tyr Leu Tyr Thr Asp Asp Ala Gln Gln Thr Glu Ala His
1 5 10 15

<210> 8
<211> 15
<212> PRT
<213> Homo sapiens

<400> 8
His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg
1 5 10 15

<210> 9
<211> 218
<212> PRT
<213> Mus musculus

<400> 9

Met	Ala	Arg	Lys	Trp	Asn	Gly	Arg	Ala	Val	Ala	Arg	Ala	Leu	Val	Leu
1			5					10					15		
Ala	Thr	Leu	Trp	Leu	Ala	Val	Ser	Gly	Arg	Pro	Leu	Ala	Gln	Gln	Ser
			20				25						30		
Gln	Ser	Val	Ser	Asp	Glu	Asp	Pro	Leu	Phe	Leu	Tyr	Gly	Trp	Gly	Lys
			35				40					45			
Ile	Thr	Arg	Leu	Gln	Tyr	Leu	Tyr	Ser	Ala	Gly	Pro	Tyr	Val	Ser	Asn
			50				55				60				
Cys	Phe	Leu	Arg	Ile	Arg	Ser	Asp	Gly	Ser	Val	Asp	Cys	Glu	Glu	Asp
	65				70				75			80			
Gln	Asn	Glu	Arg	Asn	Leu	Leu	Glu	Phe	Arg	Ala	Val	Ala	Leu	Thr	
					85				90			95			
Ile	Ala	Ile	Lys	Asp	Val	Ser	Ser	Val	Arg	Tyr	Leu	Cys	Met	Ser	Ala
					100			105				110			
Asp	Gly	Lys	Ile	Tyr	Gly	Leu	Ile	Arg	Tyr	Ser	Glu	Glu	Asp	Cys	Thr
	115					120					125				
Phe	Arg	Glu	Glu	Met	Asp	Cys	Leu	Gly	Tyr	Asn	Gln	Tyr	Arg	Ser	Met
	130					135					140				
Lys	His	His	Leu	His	Ile	Ile	Phe	Ile	Gln	Ala	Lys	Pro	Arg	Glu	Gln
	145					150			155			160			
Leu	Gln	Asp	Gln	Lys	Pro	Ser	Asn	Phe	Ile	Pro	Val	Phe	His	Arg	Ser
					165				170			175			
Phe	Phe	Glu	Thr	Gly	Asp	Gln	Leu	Arg	Ser	Lys	Met	Phe	Ser	Leu	Pro
			180				185					190			
Leu	Glu	Ser	Asp	Ser	Met	Asp	Pro	Phe	Arg	Met	Val	Glu	Asp	Val	Asp
	195					200					205				
His	Leu	Val	Lys	Ser	Pro	Ser	Phe	Gln	Lys						
	210					215									

<210> 10

<211> 216

<212> PRT

<213> Homo sapiens

<400> 10

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
1					5			10				15			
Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
						20		25				30			
His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
						35		40			45				
Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
						50		55			60				
Asp	Gly	Val	Val	Asp	Cys	Ala	Arg	Gly	Gln	Ser	Ala	His	Ser	Leu	Leu
	65					70			75			80			
Glu	Ile	Lys	Ala	Val	Ala	Leu	Arg	Thr	Val	Ala	Ile	Lys	Gly	Val	His
						85		90				95			
Ser	Val	Arg	Tyr	Leu	Cys	Met	Gly	Ala	Asp	Gly	Lys	Met	Gln	Gly	Leu
						100		105			110				
Leu	Gln	Tyr	Ser	Glu	Glu	Asp	Cys	Ala	Phe	Glu	Glu	Ile	Arg	Pro	
						115		120			125				

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
130 135 140
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
145 150 155 160
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
165 170 175
Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
180 185 190
Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
195 200 205
Val Arg Ser Pro Ser Phe Glu Lys
210 215

<210> 11
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Residues which contain the antigenic determinant
recognized by the myc monoclonal antibody.

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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 12
<211> 5
<212> PRT
<213> Unknown

<220>
<223> Preferred thrombin cleave site.

<400> 12
Leu Val Pro Arg Gly
1 5

<210> 13
<211> 10
<212> PRT
<213> Unknown

<220>
<223> Residues which bind to paramagnetic streptavidin
beads (used for purification).

<400> 13
Ser Ala Trp Arg His Pro Gln Phe Gly Gly
1 5 10

<210> 14
<211> 7
<212> PRT
<213> Homo sapiens

<400> 14
Arg Pro Tyr Asp Gly Tyr Asn
1 5

<210> 15
<211> 6
<212> PRT
<213> Homo sapiens

<400> 15
Leu Pro Met Leu Pro Met
1 5

<210> 16
<211> 6
<212> PRT
<213> Homo sapiens

<400> 16
Arg Pro Asp Gly Tyr Asn
1 5

<210> 17
<211> 6
<212> PRT
<213> Homo sapiens

<400> 17
His Phe Leu Pro Met Leu
1 5